



15

## SEQUENCE LISTING

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<110> Pompejus, Markus  
Doval, Jose Luis Revuelta  
Garcia, Maria Angeles Santos

<120> orotidine-5'-phosphate decarboxylase gene, gene construct comprising this gene and its use.

<140> US 09/582,779  
<141> 2000-07-03

<150> Germany/19801120.2  
<151> 1998-01-15

<160> 6

<170> WordPerfect version 6.1

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<213> Ashbya gossypii

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catacattct gatggtagt gctccacatc acagtaagca tttgtataag gctgatcaca 180  
tagggtgcta ccgaccttagc cattgccac atg tca acg aaa tct tac gca gaa 233  
Met Ser Thr Lys Ser Tyr Ala Glu  
1 5

agg gcc aag gca cac aat tcg cca gtt gct aga aag ctt ctg gca ttg 281  
Arg Ala Lys Ala His Asn Ser Pro Val Ala Arg Lys Leu Leu Ala Leu  
10 15 20

atg cac gag aag aaa acc aat ctc tgc gct tcc ctt gat gtg cgg acg 329  
Met His Glu Lys Lys Thr Asn Leu Cys Ala Ser Leu Asp Val Arg Thr  
25 30 35 40

tct aga aag ctt ctg gag cta gca gac acg ctg gga ccg cac att tgt 377  
Ser Arg Lys Leu Leu Glu Leu Ala Asp Thr Leu Gly Pro His Ile Cys  
45 50 55 60

ctg ctg aag aca cat gtc gac ata ctg acg gac ttc gac atc gag acg 425

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MAR 26 2001  
377

Leu Leu Lys Thr His Val Asp Ile Leu Thr Asp Phe Asp Ile Glu Thr			
60	65	70	
aca gtc aag ccg ctg cag cag ctt gcg gct aag cac aac ttc atg atc			473
Thr Val Lys Pro Leu Gln Gln Leu Ala Ala Lys His Asn Phe Met Ile			
75	80	85	
ttc gag gac cgc aag ttc gct gac att ggc aac acg gtt aag ctg cag			521
Phe Glu Asp Arg Lys Phe Ala Asp Ile Gly Asn Thr Val Lys Leu Gln			
90	95	100	
tac tcc tcc ggc gtg tac cgt atc gcg gag tgg gcg gat att acc aat			569
Tyr Ser Ser Gly Val Tyr Arg Ile Ala Glu Trp Ala Asp Ile Thr Asn			
105	110	115	120
gca cac ggc gtc acc ggc ccc ggt gtg ata gcc ggg ctg aag gag gct			617
Ala His Gly Val Thr Gly Pro Gly Val Ile Ala Gly Leu Lys Glu Ala			
125	130	135	
gcg aaa ctg gcc tca cag gaa ccc agg ggg ttg ctg atg ctg gca gag			665
Ala Lys Leu Ala Ser Gln Glu Pro Arg Gly Leu Leu Met Leu Ala Glu			
140	145	150	
ctc tct tct cag ggc tct ttg gcg cgc gga gac tat acc gcg ggc gtc			713
Leu Ser Ser Gln Gly Ser Leu Ala Arg Gly Asp Tyr Thr Ala Gly Val			
155	160	165	
gtt gaa atg gcg aag ctg gac gaa gac ttt gtg atc ggg ttc atc gcg			761
Val Glu Met Ala Lys Leu Asp Glu Asp Phe Val Ile Gly Phe Ile Ala			
170	175	180	
cag cgt gac atg ggt ggg cgt gca gac ggc ttt gac tgg ctc atc atg			809
Gln Arg Asp Met Gly Arg Ala Asp Gly Phe Asp Trp Leu Ile Met			
185	190	195	200
acc ccg ggg gtt ggc ctg gac gac aaa gga gac ggc ctg ggc cag cag			857
Thr Pro Gly Val Gly Leu Asp Asp Lys Gly Asp Gly Leu Gly Gln Gln			
205	210	215	
tac cgc acg gtg gat gag gtc gtc agc gac ggt acc gat gtg atc att			905
Tyr Arg Thr Val Asp Glu Val Val Ser Asp Gly Thr Asp Val Ile Ile			
220	225	230	
gtt ggc aga ggg ctc ttt gac aag gga aga gac ccc aag gtc gag ggt			953
Val Gly Arg Gly Leu Phe Asp Lys Gly Arg Asp Pro Lys Val Glu Gly			
235	240	245	
gcc cgc tac cgc aag gcc ggt tgg gag gct tac ttg cgc cgt atg ggc			1001
Ala Arg Tyr Arg Lys Ala Gly Trp Glu Ala Tyr Leu Arg Arg Met Gly			
250	255	260	
gag act tcg tagtctatcg ctggcgccca cagtatatag gcgattcca			1050
Glu Thr Ser			

265

ccgcccatta ccatctcagc aaccttttg taatttatatg cccctattgc ccttattcc	1110
gagctggtgc cgggatcggt ttatagacgg gcaacaagtt gatactttgt tcagtagcat	1170
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cgcacttcgt gaagtattgc tttatgaaaa atcttcactt tgggctaact agagccataa	1290
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&lt;211&gt; 267

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 1 5 10 15

val Ala Arg Lys Leu Leu Ala Leu Met His Glu Lys Lys Thr Asn Leu  
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Cys Ala Ser Leu Asp Val Arg Thr Ser Arg Lys Leu Leu Glu Leu Ala  
 35 40 45

Asp Thr Leu Gly Pro His Ile Cys Leu Leu Lys Thr His Val Asp Ile  
 50 55 60

Leu Thr Asp Phe Asp Ile Glu Thr Thr Val Lys Pro Leu Gln Gln Leu  
 65 70 75 80

Ala Ala Lys His Asn Phe Met Ile Phe Glu Asp Arg Lys Phe Ala Asp  
 85 90 95

Ile Gly Asn Thr Val Lys Leu Gln Tyr Ser Ser Gly Val Tyr Arg Ile  
 100 105 110

Ala Glu Trp Ala Asp Ile Thr Asn Ala His Gly Val Thr Gly Pro Gly  
 115 120 125

Val Ile Ala Gly Leu Lys Glu Ala Ala Lys Leu Ala Ser Gln Glu Pro  
 130 135 140

Arg Gly Leu Leu Met Leu Ala Glu Leu Ser Ser Gln Gly Ser Leu Ala  
 145 150 155 160

Arg Gly Asp Tyr Thr Ala Gly Val Val Glu Met Ala Lys Leu Asp Glu

165

170

175

Asp Phe Val Ile Gly Phe Ile Ala Gln Arg Asp Met Gly Gly Arg Ala  
 180 185 190

Asp Gly Phe Asp Trp Leu Ile Met Thr Pro Gly Val Gly Leu Asp Asp  
 195 200 205

Lys Gly Asp Gly Leu Gly Gln Gln Tyr Arg Thr Val Asp Glu Val Val  
 210 215 220

Ser Asp Gly Thr Asp Val Ile Ile Val Gly Arg Gly Leu Phe Asp Lys  
 225 230 235 240

Gly Arg Asp Pro Lys Val Glu Gly Ala Arg Tyr Arg Lys Ala Gly Trp  
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Glu Ala Tyr Leu Arg Arg Met Gly Glu Thr Ser  
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&lt;211&gt; 18

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&lt;222&gt; 1 ... 18

&lt;223&gt; n represents g, a, t or c

&lt;220&gt;

&lt;223&gt; oligonucleotide as primer for PCR

&lt;400&gt; 3

ytnggnccnt ayathtgty

18

&lt;210&gt; 4

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Unknown

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&lt;222&gt; 1 ... 23

&lt;223&gt; n represents g, a, t or c

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&lt;400&gt; 4

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23

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26

C/  
Cmt  
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gcnarnarna rnarnccnc

19--.